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Sequence Listing was accepted.

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Reviewer: Keisha Douglas

Timestamp: [year=2008; month=11; day=18; hr=14; min=57; sec=10; ms=436;
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Application No: 10582557 Version No: 2.0

Input Set:

Output Set:

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Finished: 2008-10-21 16:01:22.900
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Total Warnings: 2
Total Errors: 0
No. of SeqIDs Defined: 9
Actual SeqID Count: 9

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)

SEQUENCE LISTING

<110> KALAJI, MAHER
WILLIAMS, PETER ANTHONY
GWENIN, CHRISTOPHER DAVID

<120> IMPROVEMENTS IN AND RELATING TO BIOSENSORS

<130> 31229-232367

<140> 10582557

<141> 2008-10-21

<150> PCT/GB2004/004817

<151> 2004-11-17

<150> GB 0328784.4

<151> 2003-12-11

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<170> PatentIn version 3.5

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<213> Escherichia coli

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<223> K12

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gccaaatccg ctgccggtaa ttacgtgttc aacgagcgta aaatgcttga tgcctcgcac	240
gtcgtggtgt tctgtgcaaa aaccgcgatg gacgatgtct ggctgaagct ggttgttgac	300
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gcggtagcca tcgaaggttt tgacgcgcgc atcctcgatg cagaatttgg tctgaaagag	540
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1 5	
cac agc agc gcc ctg gtg ccg cgc gcc agc cat atg gct agc atg act	162

His	Ser	Ser	Gly	Leu	Val	Pro	Arg	Gly	Ser	His	Met	Ala	Ser	Met	Thr	
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ggt	gga	cag	caa	atg	ggt	cgc	gga	tcc	tgt	tgc	tgt	tgc	tgt	tgc	gat	210
Gly	Gly	Gln	Gln	Met	Gly	Arg	Gly	Ser	Cys	Cys	Cys	Cys	Cys	Cys	Asp	
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Ile	Ile	Ser	Val	Ala	Leu	Lys	Arg	His	Ser	Thr	Lys	Ala	Phe	Asp	Ala	
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agc	aaa	aaa	ctt	acc	ccg	gaa	cag	gcc	gag	cag	atc	aaa	acg	cta	ctg	306
Ser	Lys	Lys	Leu	Thr	Pro	Glu	Gln	Ala	Glu	Gln	Ile	Lys	Thr	Leu	Leu	
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caa	tac	agc	cca	tcc	agc	acc	aac	tcc	cag	ccg	tgg	cat	ttt	att	gtt	354
Gln	Tyr	Ser	Pro	Ser	Ser	Thr	Asn	Ser	Gln	Pro	Trp	His	Phe	Ile	Val	
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Ala	Ser	Thr	Glu	Glu	Gly	Lys	Ala	Arg	Val	Ala	Lys	Ser	Ala	Ala	Gly	
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aat	tac	gtg	ttc	aac	gag	cgt	aaa	atg	ctt	gat	gcc	tcg	cac	gtc	gtg	450
Asn	Tyr	Val	Phe	Asn	Glu	Arg	Lys	Met	Leu	Asp	Ala	Ser	His	Val	Val	
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gtg	ttc	tgt	gca	aaa	acc	gcg	atg	gac	gat	gtc	tgg	ctg	aag	ctg	gtt	498
Val	Phe	Cys	Ala	Lys	Thr	Ala	Met	Asp	Asp	Val	Trp	Leu	Lys	Leu	Val	
			125					130					135			
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Val	Asp	Gln	Glu	Asp	Ala	Asp	Gly	Arg	Phe	Ala	Thr	Pro	Glu	Ala	Lys	
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gcc	gcg	aac	gat	aaa	ggt	cgc	aag	ttc	ttc	gct	gat	atg	cac	cgt	aaa	594
Ala	Ala	Asn	Asp	Lys	Gly	Arg	Lys	Phe	Phe	Ala	Asp	Met	His	Arg	Lys	
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gat	ctg	cat	gat	gat	gca	gag	tgg	atg	gca	aaa	cag	gtt	tat	ctc	aac	642
Asp	Leu	His	Asp	Asp	Ala	Glu	Trp	Met	Ala	Lys	Gln	Val	Tyr	Leu	Asn	
170					175				180					185		
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Val	Gly	Asn	Phe	Leu	Leu	Gly	Val	Ala	Ala	Leu	Gly	Leu	Asp	Ala	Val	
				190					195					200		
ccc	atc	gaa	ggt	ttt	gac	gcc	gcc	atc	ctc	gat	gca	gaa	ttt	ggt	ctg	738
Pro	Ile	Glu	Gly	Phe	Asp	Ala	Ala	Ile	Leu	Asp	Ala	Glu	Phe	Gly	Leu	
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aaa	gag	aaa	ggc	tac	acc	agt	ctg	gtg	gtt	gtt	ccg	gta	ggt	cat	cac	786
Lys	Glu	Lys	Gly	Tyr	Thr	Ser	Leu	Val	Val	Val	Pro	Val	Gly	His	His	
		220					225					230				
agc	gtt	gaa	gat	ttt	aac	gct	acg	ctg	ccg	aaa	tct	cgt	ctg	ccg	caa	834
Ser	Val	Glu	Asp	Phe	Asn	Ala	Thr	Leu	Pro	Lys	Ser	Arg	Leu	Pro	Gln	

235	240	245	
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Asn Ile Thr Leu Thr Glu Val			
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ttctctcag attctctga ttgcataac cctgtttcag caagcttcgt catcataggc			948
tgtctgttgaa gcttgcgggc gcactcgagc accaccacca ccaccactga gatccggctg			1008
ctaacaaagc ccgaaaggaa gctgagttgg ctgctgccac cgetgagcaa taactagc			1066

Gly Arg Phe Ala Thr Pro Glu Ala Lys Ala Ala Asn Asp Lys Gly Arg
 145 150 155 160

Lys Phe Phe Ala Asp Met His Arg Lys Asp Leu His Asp Asp Ala Glu
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Trp Met Ala Lys Gln Val Tyr Leu Asn Val Gly Asn Phe Leu Leu Gly
 180 185 190

Val Ala Ala Leu Gly Leu Asp Ala Val Pro Ile Glu Gly Phe Asp Ala
 195 200 205

Ala Ile Leu Asp Ala Glu Phe Gly Leu Lys Glu Lys Gly Tyr Thr Ser
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<222> (88)..(1029)

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 1 5

cac agc agc ggc ctg gtg ccg cgc ggc agc cat atg gct agc atg act 162
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ggg gga cag caa atg ggt cgc gga tcc tgt tgc tgt tgc tgt tgc agc 210
 Gly Gly Gln Gln Met Gly Arg Gly Ser Cys Cys Cys Cys Cys Cys Ser
 30 35 40

ctt caa gac gaa gca ctc aaa gcc tgg caa gcc cgt tat ggc gag cca 258

Leu Gln Asp Glu Ala Leu Lys Ala Trp Gln Ala Arg Tyr Gly Glu Pro	
45 50 55	
gct aac tta cct gct gcc gac acc gtg atc gcg cag atg ttg cag cat	306
Ala Asn Leu Pro Ala Ala Asp Thr Val Ile Ala Gln Met Leu Gln His	
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cga tca gta cgt gcc tac agc gat ctt cct gtg gat gag cag atg ctg	354
Arg Ser Val Arg Ala Tyr Ser Asp Leu Pro Val Asp Glu Gln Met Leu	
75 80 85	
agc tgg gcg atc gcg gcg gcc cag tca gcc tcg act tcc tcg aac ctg	402
Ser Trp Ala Ile Ala Ala Ala Gln Ser Ala Ser Thr Ser Ser Asn Leu	
90 95 100 105	
caa gct tgg agc gtg ctc gcc gtg cgg gat cgc gag cgt ctc gcg agg	450
Gln Ala Trp Ser Val Leu Ala Val Arg Asp Arg Glu Arg Leu Ala Arg	
110 115 120	
ctt gcc cga ctg tcc ggt aac cag cgc cat gtc gag cag gca ccg ctg	498
Leu Ala Arg Leu Ser Gly Asn Gln Arg His Val Glu Gln Ala Pro Leu	
125 130 135	
ttc ctg gtc tgg ctc gtg gac tgg tca cgc cta cgc cga cta gcc aga	546
Phe Leu Val Trp Leu Val Asp Trp Ser Arg Leu Arg Arg Leu Ala Arg	
140 145 150	
acc ctt cag gca ccg act gca ggt atc gac tat tta gaa agc tac acc	594
Thr Leu Gln Ala Pro Thr Ala Gly Ile Asp Tyr Leu Glu Ser Tyr Thr	
155 160 165	
gtc ggt gtt gta gat gca gct ctg gcc gct cag aac gcc gca cta gct	642
Val Gly Val Val Asp Ala Ala Leu Ala Ala Gln Asn Ala Ala Leu Ala	
170 175 180 185	
ttc gag gcc caa gga ctg gga atc gtt tac atc ggc gga atg cgc aac	690
Phe Glu Ala Gln Gly Leu Gly Ile Val Tyr Ile Gly Gly Met Arg Asn	
190 195 200	
cac ccg gaa gcg atg tcc gag gag ctt ggc ctg cca aac gac act ttc	738
His Pro Glu Ala Met Ser Glu Glu Leu Gly Leu Pro Asn Asp Thr Phe	
205 210 215	
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Ala Val Phe Gly Met Cys Val Gly His Pro Asp Pro Ala Gln Pro Ala	
220 225 230	
gag atc aag cca cgc ctg gcg caa tca gtg gtg ctt cac cgt gag cgc	834
Glu Ile Lys Pro Arg Leu Ala Gln Ser Val Val Leu His Arg Glu Arg	
235 240 245	
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Tyr Glu Ala Thr Glu Ala Glu Ala Val Ser Val Ala Ala Tyr Asp Arg	
250 255 260 265	
agg atg agc gac ttc caa cat cgt caa caa cgc gaa aac cgt tcc tgg	930
Arg Met Ser Asp Phe Gln His Arg Gln Gln Arg Glu Asn Arg Ser Trp	

270	275	280	
tcc agc cag gcc gtg gaa cgt gta aaa gga gcg gat tca ctg agc gga			978
Ser Ser Gln Ala Val Glu Arg Val Lys Gly Ala Asp Ser Leu Ser Gly			
285	290	295	
aga cac cgc ttg cga gat gca tta aac acc cta ggt ttc ggc ctg cgc			1026
Arg His Arg Leu Arg Asp Ala Leu Asn Thr Leu Gly Phe Gly Leu Arg			
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Asp Leu Pro Val Asp Glu Gln Met Leu Ser Trp Ala Ile Ala Ala Ala			
85	90	95	
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115

120

125

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Gly Ile Asp Tyr Leu Glu Ser Tyr Thr Val Gly Val Val Asp Ala Ala
165 170 175

Leu Ala Ala Gln Asn Ala Ala Leu Ala Phe Glu Ala Gln Gly Leu Gly
180 185 190

Ile Val Tyr Ile Gly Gly Met Arg Asn His Pro Glu Ala Met Ser Glu
195 200 205

Glu Leu Gly Leu Pro Asn Asp Thr Phe Ala Val Phe Gly Met Cys Val
210 215 220

Gly His Pro Asp Pro Ala Gln Pro Ala Glu Ile Lys Pro Arg Leu Ala
225 230 235 240

Gln Ser Val Val Leu His Arg Glu Arg Tyr Glu Ala Thr Glu Ala Glu
245 250 255

Ala Val Ser Val Ala Ala Tyr Asp Arg Arg Met Ser Asp Phe Gln His
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Arg Gln Gln Arg Glu Asn Arg Ser Trp Ser Ser Gln Ala Val Glu Arg
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Leu Asn Thr Leu Gly Phe Gly Leu Arg
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<212> DNA

<213> Escherichia coli

<400> 7

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<210> 8

<211> 27

<212> DNA

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<211> 42

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
primer

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